## SEQUENCE LISTING

<110> OLIVER, STEPHEN P.

```
ALMEIDA, RAUL A.
     LUTHER, DOUGLAS A.
     PARK, HEE-MYUNG
<120> STREPTOCOCCUS UBERIS ADHESION MOLECULE
<130> HME/7477.0017
<140>
<141>
<150> US 60/429,499
<151> 2002-11-26
<160> 17
<170> PatentIn Ver. 2.1
<210> 1
<211> 3041
<212> DNA
<213> Streptococcus uberis
<400> 1
atgattagtc ttctatccga atttgatagt catttggtag gagtggctgt ttttgctgaa 60
aatgctaaag aagaacgtga acagatggca tataaatcat tgcttaaagt ttctgaaata 120
gatgtcaaga acaataaagt cgtcgttgaa gttgggaata tttttaacga tatataatgt 180
atggagagaa aaagggaata ttatggaatt cgaaaacaca aaatctaatc agattaaaac 240
aacacttgct ttaacgtcaa cactcgcact tcttggaact ggtgttggta tgggacatac 300
cgttaatgcg gatgacatga caactgctga tcaatcacct aaattacaag gtgaagaagc 360
aacattggcg cctacaaaca ttgaagatac taaagcagcc attgatatta aaacagctac 420
attagcagaa caaaccgatg ctcttaatac tgtaaatgag acaatcacaa gcacaaatga 480
agaattagct actttagaag gaggcttagc tgataaagaa acagcagttg cagatgctga 540
aaaaacattg gagtctgttt caaatgcctc agaagaagaa tttaatcaat tagcagaaca 600
aaataaagct gacttagcta aaactcaaga ggagctaaaa cttgctgaag caacaaaaga 660
agaagttgca acacaggtat tgacacaatc tgacgaggta acagctgcag ctaatgaagc 720
taaaaaaatg gctgaaaaag ttgcacaagc agagacaaaa gtttcagact tgacgaaaat 780
ggtcaatcaa ccagaagcaa taacagctca agttgaaata gaacaaaaca atgtcaaaat 840
catttcggaa gatttagcaa aagccaaaac tgatttagtt gctgtaacag ataatacaaa 900
aacacaatta gcaaatgatt tagcgactgc tcaatctagc ttaagtgcca aacaaaatga 960
attagctaaa gtacagtcac aaacaagtaa tgtcgcagtg aatgttatgg gtgctaataa 1020
aatggttgct ccaactaatt acccaattaa tgaaatcaaa aaattaatgt caagtggtta 1080
cattgggaca caatcttatc taaatacatt ctatgcttta aaagatcaac tggtttctaa 1140
agcagaagtt ggggcatact taaatcatta cgttgatatc gcaagtgact taaaccgtat 1200
cgttaaccca gataacttat cagttgaggt tcaaaatgaa ttggctgtat ttgcagcaac 1260
attgattaat totgttogto aacaatttgg totttotgca gtogaagtga ogcaaggtgo 1320
tcaagagttt gctcgcactt tgactcgaaa ctataaagta acacatggaa acactgttcc 1380
 tttctttaat tacaatcaac ctggcaagaa tggtcatata ggcattggtc cacacgatag 1440
 aacaattatc gaacaagcag ctacaagtgt tggcttaaaa gctaatgatg ataatatgta 1500
 tgaaaacatc ggattctttg atgatgttca tactgttaat ggtatcaaac gtagtattta 1560
taacagtatt aagtacatgc tgtttacaga cttcacctat ggaaatacat ttggacatac 1620
ggttaacttg ttgcgttctg ataaaacaaa cccaagtgct ccggtctatt taggagtttc 1680
 aacagaaact gttggtggtt taaataccca ctatgttatc ttcccggcaa gcaatattgt 1740
 aaatgccagc caattcagca aacaagtggt ttcaggtcca ttaacaacag ttgataacag 1800
```

```
tgctaaaatt agcactcttc aagcaagtat tacttctgtt gagtctaaaa ttcaaacctt 1860
acaaaaacgt attgcaaata tttcttcaga agcactagtt gtctctgcac agagaaaagt 1920
agatggttta gctgcaaaac ttcaaaaagc tgaatctaac gttgaaaaag caaaagctca 1980
acttcaacag ttacaagatt caaaagaaga tttacataaa caacttgctt tttccctttc 2040
aactcgtaag gatttaaaag gtcaacttga cgaatcgctt gttcacctaa atcagtctaa 2100
aattetttta catagettag aagaaaaaca aagteaagtg geaagteaaa ttaaegtett 2160
qacattqaaq aaqqcacaac ttqaaaaaqa actaqccttt aactctcatc caaatcgtga 2220
aaaaqttgca aaaqaaaaaq ttgaaqaggc tcaaaaaagca ttaacagaaa ccttatctca 2280
aattaaaact aaaaaagcta tcttaaatga tttaacacaa gaaaaagcaa aattgacgtc 2340
agcaatcaca acaactgaac aacaaattgt tttgttgaag aatcatttag caaatcaagt 2400
ggcgaatgct ccaaaaatca gcagtattgt ccaaagatca gaaaacaata gagtaagacc 2460
tgatgtttct gatacaagag agaaggcagt agatactgct caagaagcga caattcttgc 2520
tcaagcagaa acaatggctg aagaagtcat tacaaattct gcaaaagcca ttgttgcaaa 2580
tgctcaaaat gttgcacaag agattatgaa agtagcacct gaagtaacac ctgatcaagg 2640
agttgttgca aaagttgcag ataatattaa gaaaaataat gccccagcaa gtaaatcata 2700
tggtgcaagt tcatcaacgg taggaaatgc tacttcttca cgagatgaaa gtacaaaacg 2760
tgctttaaga gcaggaattg ttatgctggc agcagcagga cttactggtt acaaactcag 2820
aagagatggc aaaaaataag aaaatcaaag gaaaaattga ttgacagaaa gtaccgtcta 2880
tgttactata gtagacggta ctttttactt ttggtctctc aaaagtgtac agagacgtgc 2940
tgacaattgt tgcaaaagta cacacagata taggctgtca ccaagtgcta tatcaaccaa 3000
aaataaaaaa atacaggaga atgtagatgc ctacaattaa c
```

```
<210> 2
```

<211> 1007

<212> PRT

<213> Streptococcus uberis

## <400> 2

Leu Val Phe Tyr Pro Asn Leu Ile Val Ile Trp Glu Trp Leu Phe Leu

1 10 15

Leu Lys Met Leu Lys Lys Asn Val Asn Arg Trp His Ile Asn His Cys 20 25 30

Leu Lys Phe Leu Lys Met Ser Arg Thr Ile Lys Ser Ser Leu Lys Leu 35 40 45

Gly Ile Phe Leu Thr Ile Tyr Asn Val Trp Arg Glu Lys Gly Asn Ile 50 55 60

Met Glu Phe Glu Asn Thr Lys Ser Asn Gln Ile Lys Thr Thr Leu Ala 65 70 75 80

Leu Thr Ser Thr Leu Ala Leu Leu Gly Thr Gly Val Gly Met Gly His
85 90 95

Thr Val Asn Ala Asp Asp Met Thr Thr Ala Asp Gln Ser Pro Lys Leu 100 105 110

Gln Gly Glu Glu Ala Thr Leu Ala Pro Thr Asn Ile Glu Asp Thr Lys 115 120 125

Ala Ala Ile Asp Ile Lys Thr Ala Thr Leu Ala Glu Gln Thr Asp Ala 130 135 140

- Leu Asn Thr Val Asn Glu Thr Ile Thr Ser Thr Asn Glu Glu Leu Ala 145 150 155 160
- Thr Leu Glu Gly Gly Leu Ala Asp Lys Glu Thr Ala Val Ala Asp Ala 165 170 175
- Glu Lys Thr Leu Glu Ser Val Ser Asn Ala Ser Glu Glu Glu Phe Asn 180 185 190
- Gln Leu Ala Glu Gln Asn Lys Ala Asp Leu Ala Lys Thr Gln Glu Glu 195 200 205
- Leu Lys Leu Ala Glu Ala Thr Lys Glu Glu Val Ala Thr Gln Val Leu 210 215 220
- Thr Gln Ser Asp Glu Val Thr Ala Ala Ala Asn Glu Ala Lys Lys Met 225 230 235 240
- Ala Glu Lys Val Ala Gln Ala Glu Thr Lys Val Ser Asp Leu Thr Lys 245 250 255
- Met Val Asn Gln Pro Glu Ala Ile Thr Ala Gln Val Glu Ile Glu Gln 260 265 270
- Asn Asn Val Lys Ile Ile Ser Glu Asp Leu Ala Lys Ala Lys Thr Asp 275 280 285
- Leu Val Ala Val Thr Asp Asn Thr Lys Thr Gln Leu Ala Asn Asp Leu 290 295 300
- Ala Thr Ala Gln Ser Ser Leu Ser Ala Lys Gln Asn Glu Leu Ala Lys 305 310 315 320
- Val Gln Ser Gln Thr Ser Asn Val Ala Val Asn Val Met Gly Ala Asn 325 330 335
- Lys Met Val Ala Pro Thr Asn Tyr Pro Ile Asn Glu Ile Lys Lys Leu 340 345 350
- Met Ser Ser Gly Tyr Ile Gly Thr Gln Ser Tyr Leu Asn Thr Phe Tyr 355 360 365
- Ala Leu Lys Asp Gln Leu Val Ser Lys Ala Glu Val Gly Ala Tyr Leu 370 375 380
- Asn His Tyr Val Asp Ile Ala Ser Asp Leu Asn Arg Ile Val Asn Pro 385 390 395 400
- Asp Asn Leu Ser Val Glu Val Gln Asn Glu Leu Ala Val Phe Ala Ala 405 410 415
- Thr Leu Ile Asn Ser Val Arg Gln Gln Phe Gly Leu Ser Ala Val Glu
  420 425 430
- Val Thr Gln Gly Ala Gln Glu Phe Ala Arg Thr Leu Thr Arg Asn Tyr 435 440 445

- Lys Val Thr His Gly Asn Thr Val Pro Phe Phe Asn Tyr Asn Gln Pro 450 455 460
- Gly Lys Asn Gly His Ile Gly Ile Gly Pro His Asp Arg Thr Ile Ile 465 470 475 480
- Glu Gln Ala Ala Thr Ser Val Gly Leu Lys Ala Asn Asp Asp Asn Met
  485 490 495
- Tyr Glu Asn Ile Gly Phe Phe Asp Asp Val His Thr Val Asn Gly Ile
  500 505 510
- Lys Arg Ser Ile Tyr Asn Ser Ile Lys Tyr Met Leu Phe Thr Asp Phe 515 520 525
- Thr Tyr Gly Asn Thr Phe Gly His Thr Val Asn Leu Leu Arg Ser Asp 530 535
- Lys Thr Asn Pro Ser Ala Pro Val Tyr Leu Gly Val Ser Thr Glu Thr 545 550 555 560
- Val Gly Gly Leu Asn Thr His Tyr Val Ile Phe Pro Ala Ser Asn Ile 565 570 575
- Val Asn Ala Ser Gln Phe Ser Lys Gln Val Val Ser Gly Pro Leu Thr 580 585 590
- Thr Val Asp Asn Ser Ala Lys Ile Ser Thr Leu Gln Ala Ser Ile Thr 595 600 605
- Ser Val Glu Ser Lys Ile Gln Thr Leu Gln Lys Arg Ile Ala Asn Ile 610 615 620
- Ser Ser Glu Ala Leu Val Val Ser Ala Gln Arg Lys Val Asp Gly Leu 625 630 635 640
- Ala Ala Lys Leu Gln Lys Ala Glu Ser Asn Val Glu Lys Ala Lys Ala 645 650 655
- Gln Leu Gln Gln Leu Gln Asp Ser Lys Glu Asp Leu His Lys Gln Leu 660 665 670
- Ala Phe Ser Leu Ser Thr Arg Lys Asp Leu Lys Gly Gln Leu Asp Glu 675 680 685
- Ser Leu Val His Leu Asn Gln Ser Lys Ile Leu Leu His Ser Leu Glu 690 695 700
- Glu Lys Gln Ser Gln Val Ala Ser Gln Ile Asn Val Leu Thr Leu Lys 705 710 715 720
- Lys Ala Gln Leu Glu Lys Glu Leu Ala Phe Asn Ser His Pro Asn Arg 725 730 735
- Glu Lys Val Ala Lys Glu Lys Val Glu Glu Ala Gln Lys Ala Leu Thr 740 745 750

Glu Thr Leu Ser Gln Ile Lys Thr Lys Lys Ala Ile Leu Asn Asp Leu
755 760 765

Thr Gln Glu Lys Ala Lys Leu Thr Ser Ala Ile Thr Thr Glu Gln 770 775 780

Gln Ile Val Leu Leu Lys Asn His Leu Ala Asn Gln Val Ala Asn Ala 785 790 795 800

Pro Lys Ile Ser Ser Ile Val Gln Arg Ser Glu Asn Asn Arg Val Arg 805 810 815

Pro Asp Val Ser Asp Thr Arg Glu Lys Ala Val Asp Thr Ala Gln Glu 820 825 830

Ala Thr Ile Leu Ala Gln Ala Glu Thr Met Ala Glu Glu Val Ile Thr 835 840 845

Asn Ser Ala Lys Ala Ile Val Ala Asn Ala Gln Asn Val Ala Gln Glu 850 860

Ile Met Lys Val Ala Pro Glu Val Thr Pro Asp Gln Gly Val Val Ala 865 870 875 880

Lys Val Ala Asp Asn Ile Lys Lys Asn Asn Ala Pro Ala Ser Lys Ser 885 890 895

Tyr Gly Ala Ser Ser Ser Thr Val Gly Asn Ala Thr Ser Ser Arg Asp 900 905 910

Glu Ser Thr Lys Arg Ala Leu Arg Ala Gly Ile Val Met Leu Ala Ala 915 920 925

Ala Gly Leu Thr Gly Tyr Lys Leu Arg Arg Asp Gly Lys Lys Glu Asn 930 940

Gln Arg Lys Asn Leu Thr Glu Ser Thr Val Tyr Val Thr Ile Val Asp 945 950 955 960

Gly Thr Phe Tyr Phe Trp Ser Leu Lys Ser Val Gln Arg Arg Ala Asp 965 970 975

Asn Cys Cys Lys Ser Thr His Arg Tyr Arg Leu Ser Pro Ser Ala Ile 980 985 990

Ser Thr Lys Asn Lys Lys Ile Gln Glu Asn Val Asp Ala Tyr Asn 995 1000 1005

<210> 3

<211> 2971

<212> DNA

<213> Streptococcus uberis

## <400> 3

gtcatttggt aggagtggct gtttttgctg aaaatgctaa agaagaacgt gaacagatgg 60 catataaatc attgcttaaa gtttctgaaa tagatgtcaa gaacaataaa gtcgtcgttg 120

```
aagttgggaa tatttttaac gatatataat gtatggagag aaaaagggaa tattatggaa 180
ctcgaaaaca caaaatctaa tcagattaaa acaacacttg ctttaacgtc aacactcgca 240
cttcttggaa ctggtgttgg tatgggacat accgttaatg cggatgacat gacaactgct 300
gatcaatcac ctaaattaca aggtgaagaa gcaacattgg cgcctacaaa cattgaagat 360
actaaagcag ccattgatac taaaacagct acattagcag aacaaaccga tgctcttaat 420
actgtaaatg agacaatcac aagcacaaat gaagaattag ctactttaga aggaggctta 480
gctgataaag aaacagcagt tgcagatgct gaaaaaacat tggagtctgt ttcaaatgcc 540
tcagaagaag aatttaatca attagcagaa caaaataaag ctgacttagc taaaactcaa 600
gaggagctaa aacttgctga agcaacaaaa gaagaagttg caacacaggt attgacacaa 660
tctgacgagg taacagctgc agctaatgaa gctaaaaaaa tggctgaaaa agttgcacaa 720
gcagagacaa aagtttcaga cttgacgaaa atggtcaatc aaccagaagc aataacagct 780
caagttgaaa tagaacaaaa caatgtcaaa atcatttcgg aagatttagc aaaagccaaa 840
actgatttag ttgctgtaac agataataca aaaacacaat tagcaaatga tttagcgact 900
gctcaatcta gcttaagtgc caaacaaaat gaattagcta aagtacagtc acaaacaagt 960
aatgtegeag tgaatgttat gggtgetaat aaaatggttg etecaactaa ttacccaatt 1020
aatgaaatca aaaaattaat gtcaagtggt tacattggga cacaatctta tctaaataca 1080
ttctatgctt taaaagatca actggtttct aaagcagaag ttggggcata cttaaatcat 1140
tacgttgata tcgcaagtga cttaaaccgt atcgttaacc cagataactt atcagttgag 1200
gttcaaaatg aattggctgt atttgcagca acattgatta attctgttcg tcagcaattt 1260
ggtctttctg cagtcgaagt gacgcaaggt gctcaagagt ttgctcgcac tttgactcaa 1320
aactataaag caacacatgg aaacactgtt cctttcttta attacaatca acctggcaag 1380
aatggtcata taggcattgg tccacacgat agaacaatta tcgaacaagc agctacaagt 1440
gttggcttaa aagctaatga tgataacatg tatgaaaaca tcggattctt tgatgatgtt 1500
catactgtta atggtatcaa acgtagtatt tataacagta ttaagtacat gctgtttaca 1560
gacctcacct atggaaatac atttggacat acggttaact tgttgcgttc tgataaaaca 1620
aacccaagtg ctccggtcta tttaggagtt tcaacagaaa ctgttggtgg tttaaatacc 1680
cactatgtta tettecegge aagcaatatt gtaaatgeea geeagtteag caaacaagtg 1740
gtttcaggtc cattaacaac agttgataac agtgctaaaa ttagcactct tcaagcaagt 1800
attgcttctg ttgagtctaa aattcaaacc ttacaaaac gtattgcaaa tatttcttca 1860
gaagcactag ttatctctgc acagagaaaa gtagatggtt tagctgcaaa acttcaaaaa 1920
gctgaatcta acgttgaaaa agcaaaagct caacttcaac agttaaaaga ttcaaaagaa 1980
gatttacata aacaacttgc ttttgccctt tcaactcgta aggatttaaa aggtcaactt 2040
gacgaatcgc ttgttcacct aaatcagtct aaaattcttt ttcatagctt agaagaaaaa 2100
 caaagtcaag tggcaagtca aattaacgtc ttgacattga agaaggcaca acttgaaaaa 2160
 gaactageet ttaactetea tecaaategt gaaaaagttg caaaagaaaa agttgaagag 2220
 gctcaaaaag cattaacaga aaccttatct caaattaaaa ctaaaaaagc tatcttaaat 2280
 gatttaacac aagaaaaagc aaaattgacg tcagcaatca caacaactga acaacaaatt 2340
 gttttgttga agaatcattt agcaaatcaa gtggcgaatg ctccaaaaat cagcagtatt 2400
 gtccaaagat cagaaaacaa tggagtaaga cctgatgttt ctgatacaag agagaaggca 2460
 gtagatactg ctcaagaagc gacaattctt gctcaagcag aaacaatggc tgaagaagtc 2520
 attacaaatt ctgcaaaagc cattgttgca aatgctcaaa atgttgcaca agagattatg 2580
 aaagtagcac ctgaagtaac acctgatcaa ggagttgttg caaaagttgc agataatatt 2640
 aagaaaaata atgccccagc aagtaaatca tatggtgcaa gttcatcaac tgtaggaaat 2700
 gctacttctt cacgagatga aagtacaaaa cgtgctttaa gagcaggaat tgttatgctg 2760
 gcagcagcag gacttactgg ttacaaactc agaagagatg gcaaaaaata agaaaatcaa 2820
 aggaaaaatt gattgacaga aagtaccgtc tatgttacta tagtagacgg tactttttac 2880
 ttttggtctc tcaaaagtgt acagagacgt gctgacaatt gttgcaaaag tacacacaga 2940
 tataggctgt caccaagtgc tatatcaacc a
```

<sup>&</sup>lt;210> 4 <211> 15 <212> PRT <213> Streptococcus uberis

```
<400> 4
Met Thr Thr Ala Asp Gln Ser Pro Lys Leu Gln Gly Glu Glu Ala
<210> 5
<211> 45
<212> DNA
<213> Streptococcus uberis
                                                                    45
atgacaactg ctgatcaatc acctaaatta caaggtgaag aagca
<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer
<400> 6
                                                                    21
gtcatttggt aggagtggct g
 <210> 7
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Primer
 <400> 7
                                                                     23
 tggttgatat agcacttggt gac
 <210> 8
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Primer
 <400> 8
                                                                     23
 ggatgacatg acaactgctg atc
 <210> 9
 <211> 23
  <212> DNA
  <213> Artificial Sequence
  <223> Description of Artificial Sequence: Primer
```

```
<400> 9
                                                                    23
caattgtcag cacgtctctg tac
<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Primer
<400> 10
                                                                    22
cttggaactg gtgttggtat gg
<210> 11
<211> 22
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Primer
<400> 11
                                                                    22
caggtgttac ttcaggtgct ac
<210> 12
<211> 20
<212> PRT
<213> Streptococcus uberis
 <220>
 <221> MOD_RES
 <222> (17)
 <223> Thr or Ala
 <220>
 <221> MOD RES
 <222> (19)
 <223> Ile or Ala
 <220>
 <221> MOD_RES
 <222> (20)
 <223> Val or Lys
 <400> 12
 Asp Met Thr Thr Ala Asp Gln Ser Pro Lys Leu Gln Gly Glu Glu Ala
   1
 Xaa Leu Xaa Xaa
```

20

```
<210> 13
<211> 3
<212> PRT
<213> Streptococcus uberis
<400> 13
Val Ile Trp
 1
<210> 14
<211> 26
<212> PRT
<213> Streptococcus uberis
<400> 14
Glu Trp Leu Phe Leu Leu Lys Met Leu Lys Lys Asn Val Asn Arg Trp
His Ile Asn His Cys Leu Lys Phe Leu Lys
             20
<210> 15
<211> 905
<212> PRT
<213> Streptococcus uberis
<400> 15
Met Ser Arg Thr Ile Lys Ser Ser Leu Lys Leu Gly Ile Phe Leu Thr
Ile Tyr Asn Val Trp Arg Glu Lys Gly Asn Ile Met Glu Leu Glu Asn
 Thr Lys Ser Asn Gln Ile Lys Thr Thr Leu Ala Leu Thr Ser Thr Leu
Ala Leu Leu Gly Thr Gly Val Gly Met Gly His Thr Val Asn Ala Asp
 Asp Met Thr Thr Ala Asp Gln Ser Pro Lys Leu Gln Gly Glu Glu Ala
                      70
 Thr Leu Ala Pro Thr Asn Ile Glu Asp Thr Lys Ala Ala Ile Asp Thr
                                      90
 Lys Thr Ala Thr Leu Ala Glu Gln Thr Asp Ala Leu Asn Thr Val Asn
                                 105
             100
 Glu Thr Ile Thr Ser Thr Asn Glu Glu Leu Ala Thr Leu Glu Gly Gly
 Leu Ala Asp Lys Glu Thr Ala Val Ala Asp Ala Glu Lys Thr Leu Glu
```

135

- Ser Val Ser Asn Ala Ser Glu Glu Glu Phe Asn Gln Leu Ala Glu Gln 145 150 155 160
- Asn Lys Ala Asp Leu Ala Lys Thr Gln Glu Glu Leu Lys Leu Ala Glu 165 170 175
- Ala Thr Lys Glu Glu Val Ala Thr Gln Val Leu Thr Gln Ser Asp Glu 180 185 190
- Val Thr Ala Ala Ala Asn Glu Ala Lys Lys Met Ala Glu Lys Val Ala 195 200 205
- Gln Ala Glu Thr Lys Val Ser Asp Leu Thr Lys Met Val Asn Gln Pro 210 215 220
- Glu Ala Ile Thr Ala Gln Val Glu Ile Glu Gln Asn Asn Val Lys Ile 225 230 235 240
- Ile Ser Glu Asp Leu Ala Lys Ala Lys Thr Asp Leu Val Ala Val Thr 245 250 255
- Asp Asn Thr Lys Thr Gln Leu Ala Asn Asp Leu Ala Thr Ala Gln Ser 260 265 270
- Ser Leu Ser Ala Lys Gln Asn Glu Leu Ala Lys Val Gln Ser Gln Thr 275 280 285
- Ser Asn Val Ala Val Asn Val Met Gly Ala Asn Lys Met Val Ala Pro 290 295 300
- Thr Asn Tyr Pro Ile Asn Glu Ile Lys Lys Leu Met Ser Ser Gly Tyr 305 310 315 320
- Ile Gly Thr Gln Ser Tyr Leu Asn Thr Phe Tyr Ala Leu Lys Asp Gln 325 330 335
- Leu Val Ser Lys Ala Glu Val Gly Ala Tyr Leu Asn His Tyr Val Asp 340 345 350
- Ile Ala Ser Asp Leu Asn Arg Ile Val Asn Pro Asp Asn Leu Ser Val 355 360 365
- Glu Val Gln Asn Glu Leu Ala Val Phe Ala Ala Thr Leu Ile Asn Ser 370 375 380
- Val Arg Gln Gln Phe Gly Leu Ser Ala Val Glu Val Thr Gln Gly Ala 385 390 395 400
- Gln Glu Phe Ala Arg Thr Leu Thr Gln Asn Tyr Lys Ala Thr His Gly
  405 410 415
- Asn Thr Val Pro Phe Phe Asn Tyr Asn Gln Pro Gly Lys Asn Gly His 420 425 430
- Ile Gly Ile Gly Pro His Asp Arg Thr Ile Ile Glu Gln Ala Ala Thr 435 440 445

- Ser Val Gly Leu Lys Ala Asn Asp Asp Asn Met Tyr Glu Asn Ile Gly 450 455 460
- Phe Phe Asp Asp Val His Thr Val Asn Gly Ile Lys Arg Ser Ile Tyr 465 470 475 480
- Asn Ser Ile Lys Tyr Met Leu Phe Thr Asp Leu Thr Tyr Gly Asn Thr 485 490 495
- Phe Gly His Thr Val Asn Leu Leu Arg Ser Asp Lys Thr Asn Pro Ser 500 505 510
- Ala Pro Val Tyr Leu Gly Val Ser Thr Glu Thr Val Gly Gly Leu Asn 515 520 525
- Thr His Tyr Val Ile Phe Pro Ala Ser Asn Ile Val Asn Ala Ser Gln 530 540
- Phe Ser Lys Gln Val Val Ser Gly Pro Leu Thr Thr Val Asp Asn Ser 545 550 555
- Ala Lys Ile Ser Thr Leu Gln Ala Ser Ile Ala Ser Val Glu Ser Lys 565 570 575
- Ile Gln Thr Leu Gln Lys Arg Ile Ala Asn Ile Ser Ser Glu Ala Leu 580 585 590
- Val Ile Ser Ala Gln Arg Lys Val Asp Gly Leu Ala Ala Lys Leu Gln 595 600 605
- Lys Ala Glu Ser Asn Val Glu Lys Ala Lys Ala Gln Leu Gln Gln Leu 610 615 620
- Lys Asp Ser Lys Glu Asp Leu His Lys Gln Leu Ala Phe Ala Leu Ser 625 630 635 640
- Thr Arg Lys Asp Leu Lys Gly Gln Leu Asp Glu Ser Leu Val His Leu 645 650 655
- Asn Gln Ser Lys Ile Leu Phe His Ser Leu Glu Glu Lys Gln Ser Gln 660 665 670
- Val Ala Ser Gln Ile Asn Val Leu Thr Leu Lys Lys Ala Gln Leu Glu 675 680 685
- Lys Glu Leu Ala Phe Asn Ser His Pro Asn Arg Glu Lys Val Ala Lys 690 695 700
- Glu Lys Val Glu Glu Ala Gln Lys Ala Leu Thr Glu Thr Leu Ser Gln 705 710 715 720
- Ile Lys Thr Lys Lys Ala Ile Leu Asn Asp Leu Thr Gln Glu Lys Ala 725 730 735
- Lys Leu Thr Ser Ala Ile Thr Thr Glu Gln Gln Ile Val Leu Leu 740 745 750

Lys Asn His Leu Ala Asn Gln Val Ala Asn Ala Pro Lys Ile Ser Ser 755 760 765

Ile Val Gln Arg Ser Glu Asn Asn Gly Val Arg Pro Asp Val Ser Asp 770 785

Thr Arg Glu Lys Ala Val Asp Thr Ala Gln Glu Ala Thr Ile Leu Ala 785 790 795 800

Gln Ala Glu Thr Met Ala Glu Glu Val Ile Thr Asn Ser Ala Lys Ala 805 810 815

Ile Val Ala Asn Ala Gln Asn Val Ala Gln Glu Ile Met Lys Val Ala 820 825 830

Pro Glu Val Thr Pro Asp Gln Gly Val Val Ala Lys Val Ala Asp Asn 835 840 845

Ile Lys Lys Asn Asn Ala Pro Ala Ser Lys Ser Tyr Gly Ala Ser Ser 850 860

Ser Thr Val Gly Asn Ala Thr Ser Ser Arg Asp Glu Ser Thr Lys Arg 865 870 875 880

Ala Leu Arg Ala Gly Ile Val Met Leu Ala Ala Gly Leu Thr Gly 885 890 895

Tyr Lys Leu Arg Arg Asp Gly Lys Lys 900 905

<210> 16

<211> 6

<212> PRT

<213> Streptococcus uberis

<400> 16

Glu Asn Gln Arg Lys Asn 1 5

<210> 17

<211> 46

<212> PRT

<213> Streptococcus uberis

<400> 17

Leu Thr Glu Ser Thr Val Tyr Val Thr Ile Val Asp Gly Thr Phe Tyr  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Phe Trp Ser Leu Lys Ser Val Gln Arg Arg Ala Asp Asn Cys Cys Lys
20 25 30

Ser Thr His Arg Tyr Arg Leu Ser Pro Ser Ala Ile Ser Thr
35 40 45